



1/36

SEQUENCE LISTING

<110> Gray, John T.  
Mulligan, Richard C.

<120> Packaging Cell Lines

<130> CMCC693p2A

<140> US 09/393,795

<141> 1999-09-10

<150> US 60/100,063

<151> 1998-09-12

<150> US 60/100,022

<151> 1998-09-11

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<210> 1

<211> 396

<212> DNA

<213> Homo sapien

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ttaaggccag ggggaaagaa aaaatataaa ttaaaacata tagtatgggc aagcagggag 120  
ctagaacgat tcgcagttaa tcctggcctg ttagaaacat cagaaggctg tagacaaata 180  
ctgggacagc tacaaccatc ccttcagaca ggatcagaag aacttagatc attatataat 240  
acagtagcaa ccctctattg tgtgcatcaa aggatagaga taaaagacac caaggaagct 300  
ttagacaaga tagaggaaga gcaaaacaaa agtaagaaaa aagcacagca agcagcagct 360  
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<210> 2

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<212> DNA

<213> Homo sapien

<220>

<221> CDS

<222> (1) ... (1503)

<400> 2

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Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Lys Trp  
1 5 10 15

gaa	aaa	att	cgg	tta	agg	cca	ggg	gga	aag	aaa	caa	tat	aaa	cta	aaa	96
Glu	Lys	Ile	Arg	Leu	Arg	Pro	Gly	Gly	Lys	Lys	Gln	Tyr	Lys	Leu	Lys	
			20				25						30			
cat	ata	gta	tgg	gca	agc	agg	gag	cta	gaa	cga	ttc	gca	gtt	aat	cct	144
His	Ile	Val	Trp	Ala	Ser	Arg	Glu	Leu	Glu	Arg	Phe	Ala	Val	Asn	Pro	
		35					40					45				
ggc	ctt	tta	gag	aca	tca	gaa	ggc	tgt	aga	caa	ata	ctg	gga	cag	cta	192
Gly	Leu	Leu	Glu	Thr	Ser	Glu	Gly	Cys	Arg	Gln	Ile	Leu	Gly	Gln	Leu	
	50					55					60					
caa	cca	tcc	ctt	cag	aca	gga	tca	gaa	gaa	ctt	aga	tca	tta	tat	aat	240
Gln	Pro	Ser	Leu	Gln	Thr	Gly	Ser	Glu	Glu	Leu	Arg	Ser	Leu	Tyr	Asn	
65					70					75					80	
aca	ata	gca	gtc	ctc	tat	tgt	gtg	cat	caa	agg	ata	gat	gta	aaa	gac	288
Thr	Ile	Ala	Val	Leu	Tyr	Cys	Val	His	Gln	Arg	Ile	Asp	Val	Lys	Asp	
			85					90					95			
acc	aag	gaa	gcc	tta	gat	aag	ata	gag	gaa	gag	caa	aac	aaa	agt	aag	336
Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu	Glu	Gln	Asn	Lys	Ser	Lys	
			100					105					110			
aaa	aag	gca	cag	caa	gca	gca	gct	gac	aca	gga	aac	aac	agc	cag	gtc	384
Lys	Lys	Ala	Gln	Gln	Ala	Ala	Ala	Asp	Thr	Gly	Asn	Asn	Ser	Gln	Val	
		115					120					125				
agc	caa	aat	tac	cct	ata	gtg	cag	aac	ctc	cag	ggg	caa	atg	gta	cat	432
Ser	Gln	Asn	Tyr	Pro	Ile	Val	Gln	Asn	Leu	Gln	Gly	Gln	Met	Val	His	
	130					135					140					
cag	gcc	ata	tca	cct	aga	act	tta	aat	gca	tgg	gta	aaa	gta	gta	gaa	480
Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala	Trp	Val	Lys	Val	Val	Glu	
145					150					155					160	
gag	aag	gct	ttc	agc	cca	gaa	gta	ata	ccc	atg	ttt	tca	gca	tta	tca	528
Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro	Met	Phe	Ser	Ala	Leu	Ser	
			165					170						175		
gaa	gga	gcc	acc	cca	caa	gat	tta	aat	acc	atg	cta	aac	aca	gtg	ggg	576
Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr	Met	Leu	Asn	Thr	Val	Gly	
			180					185					190			
gga	cat	caa	gca	gcc	atg	caa	atg	tta	aaa	gag	acc	atc	aat	gag	gaa	624
Gly	His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys	Glu	Thr	Ile	Asn	Glu	Glu	
		195				200						205				
gct	gca	gaa	tgg	gat	aga	ttg	cat	cca	gtg	cat	gca	ggg	cct	att	gca	672
Ala	Ala	Glu	Trp	Asp	Arg	Leu	His	Pro	Val	His	Ala	Gly	Pro	Ile	Ala	
	210					215					220					

cca ggc cag atg aga gaa cca agg gga agt gac ata gca gga act act	720
Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr	
225 230 235 240	
agt acc ctt cag gaa caa ata gga tgg atg aca cat aat cca cct atc	768
Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr His Asn Pro Pro Ile	
245 250 255	
cca gta gga gaa atc tat aaa aga tgg ata atc ctg gga tta aat aaa	816
Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys	
260 265 270	
ata gta aga atg tat agc cct acc agc att ctg gac ata aga caa gga	864
Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly	
275 280 285	
cca aag gaa ccc ttt aga gac tat gta gac cga ttc tat aaa act cta	912
Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu	
290 295 300	
aga gcc gag caa gct tca caa gag gta aaa aat tgg atg aca gaa acc	960
Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr	
305 310 315 320	
ttg ttg gtc caa aat gcg aac cca gat tgt aag act att tta aaa gca	1008
Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala	
325 330 335	
ttg gga cca gga gcg aca cta gaa gaa atg atg aca gca tgt cag gga	1056
Leu Gly Pro Gly Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly	
340 345 350	
gtg ggg gga ccc ggc cat aaa gca aga gtt ttg gct gaa gca atg agc	1104
Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser	
355 360 365	
caa gta aca aat cca gct acc ata atg ata cag aaa ggc aat ttt agg	1152
Gln Val Thr Asn Pro Ala Thr Ile Met Ile Gln Lys Gly Asn Phe Arg	
370 375 380	
aac caa aga aag act gtt aag tgt ttc aat tgt ggc aaa gaa ggg cac	1200
Asn Gln Arg Lys Thr Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His	
385 390 395 400	
ata gcc aaa aat tgc agg gcc cct agg aaa aag ggc tgt tgg aaa tgt	1248
Ile Ala Lys Asn Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys	
405 410 415	
gga aag gaa gga cac caa atg aaa gat tgt act gag aga cag gct aat	1296
Gly Lys Glu Gly His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn	
420 425 430	

ttt	tta	ggg	aag	atc	tgg	cct	tcc	cac	aag	gga	agg	cca	ggg	aat	ttt	1344
Phe	Leu	Gly	Lys	Ile	Trp	Pro	Ser	His	Lys	Gly	Arg	Pro	Gly	Asn	Phe	
		435					440					445				

ctt	cag	agc	aga	cca	gag	cca	aca	gcc	cca	cca	gaa	gag	agc	ttc	agg	1392
Leu	Gln	Ser	Arg	Pro	Glu	Pro	Thr	Ala	Pro	Pro	Glu	Glu	Ser	Phe	Arg	
	450					455					460					

ttt	ggg	gaa	gag	aca	aca	act	ccc	tct	cag	aag	cag	gag	ccg	ata	gac	1440
Phe	Gly	Glu	Glu	Thr	Thr	Thr	Pro	Ser	Gln	Lys	Gln	Glu	Pro	Ile	Asp	
465					470					475					480	

aag	gaa	ctg	tat	cct	tta	gct	tcc	ctc	aga	tca	ctc	ttt	ggc	agc	gac	1488
Lys	Glu	Leu	Tyr	Pro	Leu	Ala	Ser	Leu	Arg	Ser	Leu	Phe	Gly	Ser	Asp	
				485					490					495		

ccc	tcg	tca	caa	taa	1503
Pro	Ser	Ser	Gln	*	
			500		

<210> 3  
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 <212> PRT  
 <213> Homo sapien

<400> 3															
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1				5					10					15	
Glu	Lys	Ile	Arg	Leu	Arg	Pro	Gly	Gly	Lys	Lys	Gln	Tyr	Lys	Leu	Lys
			20					25					30		
His	Ile	Val	Trp	Ala	Ser	Arg	Glu	Leu	Glu	Arg	Phe	Ala	Val	Asn	Pro
		35					40					45			
Gly	Leu	Leu	Glu	Thr	Ser	Glu	Gly	Cys	Arg	Gln	Ile	Leu	Gly	Gln	Leu
	50					55				60					
Gln	Pro	Ser	Leu	Gln	Thr	Gly	Ser	Glu	Glu	Leu	Arg	Ser	Leu	Tyr	Asn
65					70					75					80
Thr	Ile	Ala	Val	Leu	Tyr	Cys	Val	His	Gln	Arg	Ile	Asp	Val	Lys	Asp
			85						90					95	
Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu	Glu	Gln	Asn	Lys	Ser	Lys
			100					105					110		
Lys	Lys	Ala	Gln	Gln	Ala	Ala	Ala	Asp	Thr	Gly	Asn	Asn	Ser	Gln	Val
		115				120						125			
Ser	Gln	Asn	Tyr	Pro	Ile	Val	Gln	Asn	Leu	Gln	Gly	Gln	Met	Val	His
	130					135					140				
Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala	Trp	Val	Lys	Val	Val	Glu
145					150					155					160
Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro	Met	Phe	Ser	Ala	Leu	Ser
			165						170					175	
Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr	Met	Leu	Asn	Thr	Val	Gly
			180					185					190		

Gly	His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys	Glu	Thr	Ile	Asn	Glu	Glu
		195					200					205			
Ala	Ala	Glu	Trp	Asp	Arg	Leu	His	Pro	Val	His	Ala	Gly	Pro	Ile	Ala
		210					215				220				
Pro	Gly	Gln	Met	Arg	Glu	Pro	Arg	Gly	Ser	Asp	Ile	Ala	Gly	Thr	Thr
225					230					235					240
Ser	Thr	Leu	Gln	Glu	Gln	Ile	Gly	Trp	Met	Thr	His	Asn	Pro	Pro	Ile
			245						250					255	
Pro	Val	Gly	Glu	Ile	Tyr	Lys	Arg	Trp	Ile	Ile	Leu	Gly	Leu	Asn	Lys
		260						265					270		
Ile	Val	Arg	Met	Tyr	Ser	Pro	Thr	Ser	Ile	Leu	Asp	Ile	Arg	Gln	Gly
		275					280					285			
Pro	Lys	Glu	Pro	Phe	Arg	Asp	Tyr	Val	Asp	Arg	Phe	Tyr	Lys	Thr	Leu
	290					295					300				
Arg	Ala	Glu	Gln	Ala	Ser	Gln	Glu	Val	Lys	Asn	Trp	Met	Thr	Glu	Thr
305					310					315					320
Leu	Leu	Val	Gln	Asn	Ala	Asn	Pro	Asp	Cys	Lys	Thr	Ile	Leu	Lys	Ala
			325						330					335	
Leu	Gly	Pro	Gly	Ala	Thr	Leu	Glu	Glu	Met	Met	Thr	Ala	Cys	Gln	Gly
		340						345					350		
Val	Gly	Gly	Pro	Gly	His	Lys	Ala	Arg	Val	Leu	Ala	Glu	Ala	Met	Ser
		355					360					365			
Gln	Val	Thr	Asn	Pro	Ala	Thr	Ile	Met	Ile	Gln	Lys	Gly	Asn	Phe	Arg
	370					375					380				
Asn	Gln	Arg	Lys	Thr	Val	Lys	Cys	Phe	Asn	Cys	Gly	Lys	Glu	Gly	His
385					390					395					400
Ile	Ala	Lys	Asn	Cys	Arg	Ala	Pro	Arg	Lys	Lys	Gly	Cys	Trp	Lys	Cys
			405						410					415	
Gly	Lys	Glu	Gly	His	Gln	Met	Lys	Asp	Cys	Thr	Glu	Arg	Gln	Ala	Asn
		420						425					430		
Phe	Leu	Gly	Lys	Ile	Trp	Pro	Ser	His	Lys	Gly	Arg	Pro	Gly	Asn	Phe
	435					440						445			
Leu	Gln	Ser	Arg	Pro	Glu	Pro	Thr	Ala	Pro	Pro	Glu	Glu	Ser	Phe	Arg
	450					455					460				
Phe	Gly	Glu	Glu	Thr	Thr	Thr	Pro	Ser	Gln	Lys	Gln	Glu	Pro	Ile	Asp
465					470					475					480
Lys	Glu	Leu	Tyr	Pro	Leu	Ala	Ser	Leu	Arg	Ser	Leu	Phe	Gly	Ser	Asp
			485						490					495	
Pro	Ser	Ser	Gln												
			500												

&lt;210&gt; 4

&lt;211&gt; 1503

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Codon optimized form of HIV gag coding region

&lt;221&gt; CDS

&lt;222&gt; (1)...(1503)

&lt;400&gt; 4

atg ggc gcc cgc gcc tcc gtg ctg tcc ggc ggc gag ctg gac aag tgg	48
Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Lys Trp	
1 5 10 15	
 gag aag atc cgc ctg cgc ccc ggc ggc aag aag cag tac aag ctg aag	 96
Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Gln Tyr Lys Leu Lys	
20 25 30	
 cac atc gtg tgg gcc tcc cgc gag ctg gag cgc ttc gcc gtg aac ccc	 144
His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro	
35 40 45	
 ggc ctg ctg gag acc tcc gag ggc tgc cgc cag atc ctg ggc cag ctg	 192
Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu	
50 55 60	
 cag ccc tcc ctg caa acc ggc tcc gag gag ctg cgc tcc ctg tac aac	 240
Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn	
65 70 75 80	
 acc atc gcc gtg ctg tac tgc gtg cac cag cgc atc gac gtg aag gac	 288
Thr Ile Ala Val Leu Tyr Cys Val His Gln Arg Ile Asp Val Lys Asp	
85 90 95	
 acc aag gag gcc ctg gac aag atc gag gag gag cag aac aag tcc aag	 336
Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys	
100 105 110	
 aag aag gcc cag cag gcc gcc gcc gac acc ggc aac aac tcc cag gtg	 384
Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly Asn Asn Ser Gln Val	
115 120 125	
 tcc cag aac tac ccc atc gtg cag aac ctg cag ggc cag atg gtg cac	 432
Ser Gln Asn Tyr Pro Ile Val Gln Asn Leu Gln Gly Gln Met Val His	
130 135 140	
 cag gcc atc tcc ccc cgc acc ctg aac gcc tgg gtg aag gtg gtg gag	 480
Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu	
145 150 155 160	
 gag aag gcc ttc tcc ccc gaa gtc atc ccc atg ttc tcc gcc ctg tcc	 528
Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser	
165 170 175	
 gag ggc gcc acc ccc cag gac ctg aac acc atg ctg aac acc gtg ggc	 576
Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly	
180 185 190	

ggc cac cag gcc gcc atg cag atg ctg aag gag acc atc aac gag gag Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu 195 200 205	624
gcc gcc gag tgg gac cgc ctg cac ccc gtg cac gcc ggc ccc atc gcc Ala Ala Glu Trp Asp Arg Leu His Pro Val His Ala Gly Pro Ile Ala 210 215 220	672
ccc ggc cag atg cgc gag ccc cgc ggc tcc gac atc gcc ggc acc acc Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr 225 230 235 240	720
tcc acc ctg caa gag cag atc ggc tgg atg acc cac aac ccc ccc atc Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr His Asn Pro Pro Ile 245 250 255	768
ccc gtg ggc gag atc tac aag cgc tgg atc atc ctg ggc ctg aac aag Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys 260 265 270	816
atc gtg cgc atg tac tcc ccc acc tcc atc ctg gac atc cgc cag ggc Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly 275 280 285	864
ccc aag gag ccc ttc cgc gac tac gtg gac cgc ttc tac aag acc ctg Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu 290 295 300	912
cgc gcc gag cag gcc tcc cag gag gta aag aac tgg atg acc gag acc Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr 305 310 315 320	960
ctg ctg gtg cag aac gcc aac ccc gac tgc aag acc atc ctg aag gcc Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala 325 330 335	1008
ctg ggc ccc ggc gcc acc ctg gag gag atg atg acc gcc tgc cag ggc Leu Gly Pro Gly Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly 340 345 350	1056
gtg ggc ggc ccc ggc cac aag gcc cgc gtg ctg gcc gag gcc atg tcc Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser 355 360 365	1104
caa gtc acc aac ccc gcc acc atc atg atc cag aag ggc aac ttc cgc Gln Val Thr Asn Pro Ala Thr Ile Met Ile Gln Lys Gly Asn Phe Arg 370 375 380	1152
aac cag cgc aag acc gtg aag tgc ttc aac tgc ggc aag gag ggc cac Asn Gln Arg Lys Thr Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His 385 390 395 400	1200

atc gcc aag aac tgc cgc gcc ccc cgc aag aag ggc tgc tgg aag tgc	1248
Ile Ala Lys Asn Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys	
405 410 415	
ggc aag gag ggc cac cag atg aaa gat tgt act gag aga cag gct aat	1296
Gly Lys Glu Gly His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn	
420 425 430	
ttt tta ggg aag atc tgg cct tcc cac aag gga agg cca ggg aat ttt	1344
Phe Leu Gly Lys Ile Trp Pro Ser His Lys Gly Arg Pro Gly Asn Phe	
435 440 445	
ctt cag agc aga cca gag cca aca gcc cca cca gaa gag agc ttc agg	1392
Leu Gln Ser Arg Pro Glu Pro Thr Ala Pro Pro Glu Glu Ser Phe Arg	
450 455 460	
ttt ggg gaa gag aca aca act ccc tct cag aag cag gag ccg ata gac	1440
Phe Gly Glu Glu Thr Thr Thr Pro Ser Gln Lys Gln Glu Pro Ile Asp	
465 470 475 480	
aag gaa ctg tat cct tta gct tcc ctc aga tca ctc ttt ggc agc gac	1488
Lys Glu Leu Tyr Pro Leu Ala Ser Leu Arg Ser Leu Phe Gly Ser Asp	
485 490 495	
ccc tcg tca caa taa	1503
Pro Ser Ser Gln *	
500	

&lt;210&gt; 5

&lt;211&gt; 500

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Codon optimized form of HIV gag coding region

&lt;400&gt; 5

Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Lys Trp	
1 5 10 15	
Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Gln Tyr Lys Leu Lys	
20 25 30	
His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro	
35 40 45	
Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu	
50 55 60	
Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn	
65 70 75 80	
Thr Ile Ala Val Leu Tyr Cys Val His Gln Arg Ile Asp Val Lys Asp	
85 90 95	
Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Gln Asn Lys Ser Lys	
100 105 110	



Lys	Lys	Ala	Gln	Gln	Ala	Ala	Ala	Asp	Thr	Gly	Asn	Asn	Ser	Gln	Val	115	120	125
Ser	Gln	Asn	Tyr	Pro	Ile	Val	Gln	Asn	Leu	Gln	Gly	Gln	Met	Val	His	130	135	140
Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala	Trp	Val	Lys	Val	Val	Glu	145	150	155
Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro	Met	Phe	Ser	Ala	Leu	Ser	165	170	175
Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr	Met	Leu	Asn	Thr	Val	Gly	180	185	190
Gly	His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys	Glu	Thr	Ile	Asn	Glu	Glu	195	200	205
Ala	Ala	Glu	Trp	Asp	Arg	Leu	His	Pro	Val	His	Ala	Gly	Pro	Ile	Ala	210	215	220
Pro	Gly	Gln	Met	Arg	Glu	Pro	Arg	Gly	Ser	Asp	Ile	Ala	Gly	Thr	Thr	225	230	235
Ser	Thr	Leu	Gln	Glu	Gln	Ile	Gly	Trp	Met	Thr	His	Asn	Pro	Pro	Ile	245	250	255
Pro	Val	Gly	Glu	Ile	Tyr	Lys	Arg	Trp	Ile	Ile	Leu	Gly	Leu	Asn	Lys	260	265	270
Ile	Val	Arg	Met	Tyr	Ser	Pro	Thr	Ser	Ile	Leu	Asp	Ile	Arg	Gln	Gly	275	280	285
Pro	Lys	Glu	Pro	Phe	Arg	Asp	Tyr	Val	Asp	Arg	Phe	Tyr	Lys	Thr	Leu	290	295	300
Arg	Ala	Glu	Gln	Ala	Ser	Gln	Glu	Val	Lys	Asn	Trp	Met	Thr	Glu	Thr	305	310	315
Leu	Leu	Val	Gln	Asn	Ala	Asn	Pro	Asp	Cys	Lys	Thr	Ile	Leu	Lys	Ala	325	330	335
Leu	Gly	Pro	Gly	Ala	Thr	Leu	Glu	Glu	Met	Met	Thr	Ala	Cys	Gln	Gly	340	345	350
Val	Gly	Gly	Pro	Gly	His	Lys	Ala	Arg	Val	Leu	Ala	Glu	Ala	Met	Ser	355	360	365
Gln	Val	Thr	Asn	Pro	Ala	Thr	Ile	Met	Ile	Gln	Lys	Gly	Asn	Phe	Arg	370	375	380
Asn	Gln	Arg	Lys	Thr	Val	Lys	Cys	Phe	Asn	Cys	Gly	Lys	Glu	Gly	His	385	390	395
Ile	Ala	Lys	Asn	Cys	Arg	Ala	Pro	Arg	Lys	Lys	Gly	Cys	Trp	Lys	Cys	405	410	415
Gly	Lys	Glu	Gly	His	Gln	Met	Lys	Asp	Cys	Thr	Glu	Arg	Gln	Ala	Asn	420	425	430
Phe	Leu	Gly	Lys	Ile	Trp	Pro	Ser	His	Lys	Gly	Arg	Pro	Gly	Asn	Phe	435	440	445
Leu	Gln	Ser	Arg	Pro	Glu	Pro	Thr	Ala	Pro	Pro	Glu	Glu	Ser	Phe	Arg	450	455	460
Phe	Gly	Glu	Glu	Thr	Thr	Thr	Pro	Ser	Gln	Lys	Gln	Glu	Pro	Ile	Asp	465	470	475
Lys	Glu	Leu	Tyr	Pro	Leu	Ala	Ser	Leu	Arg	Ser	Leu	Phe	Gly	Ser	Asp	485	490	495
Pro	Ser	Ser	Gln													500		

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Arg Trp Lys Pro Lys Met Ile Gly Gly Ile Gly Gly Phe Ile Lys Val	
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Cys Thr Glu Met Glu Lys Glu Gly Lys Ile Ser Lys Ile Gly Pro Glu	
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Val Pro Leu Asp Lys Asp Phe Arg Lys Tyr Thr Ala Phe Thr Ile Pro	
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Ser Ile Asn Asn Glu Thr Pro Gly Ile Arg Tyr Gln Tyr Asn Val Leu	
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Leu Pro Glu Lys Asp Ser Trp Thr Val Asn Asp Ile Gln Lys Leu Val	
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Glu	Gly	Ala	Val	Val	Ile	Gln	Asp	Asn	Ser	Asp	Ile	Lys	Val	Val	Pro	
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Arg	Arg	Lys	Ala	Lys	Ile	Ile	Arg	Asp	Tyr	Gly	Lys	Gln	Met	Ala	Gly	
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3012

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 Arg Trp Lys Pro Lys Met Ile Gly Gly Ile Gly Gly Phe Ile Lys Val  
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 Cys Thr Glu Met Glu Lys Glu Gly Lys Ile Ser Lys Ile Gly Pro Glu  
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 Lys Trp Arg Lys Leu Val Asp Phe Arg Glu Leu Asn Lys Arg Thr Gln  
 225 230 235 240  
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 Val Pro Leu Asp Lys Asp Phe Arg Lys Tyr Thr Ala Phe Thr Ile Pro  
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 Ser Ile Asn Asn Glu Thr Pro Gly Ile Arg Tyr Gln Tyr Asn Val Leu  
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 Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe Gln Cys Ser Met Thr  
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Ala Glu Val Ile Pro Ala Glu Thr Gly Gln Glu Thr Ala Tyr Phe Leu
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Arg Gln Tyr Asp Gln Ile Leu Ile Glu Ile Cys Gly His Lys Ala Ile	
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Ser Ile Asn Asn Glu Thr Pro Gly Ile Arg Tyr Gln Tyr Asn Val Leu	
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Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser Asp Leu Glu Ile Gly Gln	
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Arg	Asp	Gln	Ala	Glu	His	Leu	Lys	Thr	Ala	Val	Gln	Met	Ala	Val	Phe	
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Gln	Lys	Gln	Ile	Thr	Lys	Ile	Gln	Asn	Phe	Arg	Val	Tyr	Tyr	Arg	Asp	
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Ser	Arg	Asp	Pro	Val	Trp	Lys	Gly	Pro	Ala	Lys	Leu	Leu	Trp	Lys	Gly	
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Cys Thr Glu Met Glu Lys Glu Gly Lys Ile Ser Lys Ile Gly Pro Glu	
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Ser Ile Asn Asn Glu Thr Pro Gly Ile Arg Tyr Gln Tyr Asn Val Leu	
290 295 300	

ccc Pro 305	cag Gln	ggc Gly	tgg Trp	aag Lys	ggc Gly	tcc Ser	ccc Pro	gcc Ala	atc Ile	ttc Phe	cag Gln	tgc Cys	tcc Ser	atg Met	acc Thr	960
				310				315				320				
aag Lys	atc Ile	ctg Leu	gag Glu	ccc Pro	ttc Phe	cgc Arg	aag Lys	cag Gln	aac Asn	ccc Pro	gac Asp	atc Ile	gtg Val	atc Ile	tac Tyr	1008
				325				330				335				
cag Gln	tac Tyr	atg Met	gac Asp	gac Asp	ctg Leu	tac Tyr	gtg Val	ggc Gly	tcc Ser	gac Asp	ctg Leu	gag Glu	atc Ile	ggc Gly	cag Gln	1056
				340				345				350				
cac His	cgc Arg	acc Thr	aag Lys	atc Ile	gag Glu	gag Glu	ctg Leu	cgc Arg	cag Gln	cac His	ctg Leu	ctg Leu	cgc Arg	tgg Trp	ggc Gly	1104
				355				360				365				
ttc Phe	acc Thr	acc Thr	ccc Pro	gac Asp	aag Lys	aag Lys	cac His	cag Gln	aag Lys	gag Glu	ccc Pro	ccc Pro	ttc Phe	ctg Leu	tgg Trp	1152
				370				375				380				
atg Met 385	ggc Gly	tac Tyr	gag Glu	ctg Leu	cac His	ccc Pro	gac Asp	aag Lys	tgg Trp	acc Thr	gtg Val	cag Gln	ccc Pro	atc Ile	gtg Val	1200
				390				395				400				
ctg Leu	ccc Pro	gag Glu	aag Lys	gac Asp	tcc Ser	tgg Trp	acc Thr	gtg Val	aac Asn	gac Asp	atc Ile	cag Gln	aag Lys	ctg Leu	gtg Val	1248
				405				410				415				
ggc Gly	aag Lys	ctg Leu	aac Asn	tgg Trp	gcc Ala	tcc Ser	cag Gln	atc Ile	tac Tyr	gcc Ala	ggc Gly	atc Ile	aaa Lys	gtc Val	cgc Arg	1296
				420				425				430				
cag Gln	ctg Leu	tgc Cys	aag Lys	ctg Leu	ctg Leu	cgc Arg	ggc Gly	acc Thr	aag Lys	gcc Ala	ctg Leu	acc Thr	gag Glu	gtg Val	gtg Val	1344
				435				440				445				
ccc Pro	ctg Leu	acc Thr	gag Glu	gag Glu	gcc Ala	gag Glu	ctg Leu	gag Glu	ctg Leu	gcc Ala	gag Glu	aac Asn	cgc Arg	gag Glu	atc Ile	1392
				450				455				460				
ctg Leu 465	aag Lys	gag Glu	ccc Pro	gtg Val	cac His	ggc Gly	gtg Val	tac Tyr	tac Tyr	gac Asp	ccc Pro	tcc Ser	aag Lys	gac Asp	ctg Leu	1440
				470				475				480				
atc Ile	gcc Ala	gag Glu	atc Ile	cag Gln	aag Lys	cag Gln	ggc Gly	cag Gln	ggc Gly	cag Gln	tgg Trp	acc Thr	tac Tyr	cag Gln	atc Ile	1488
				485				490				495				
tac Tyr	cag Gln	gag Glu	ccc Pro	ttc Phe	aag Lys	aac Asn	ctg Leu	aag Lys	acc Thr	ggc Gly	aaa Lys	tac Tyr	gcc Ala	cgc Arg	atg Met	1536
				500				505				510				

aag ggc gcc cac acc aac gac gtg aag cag ctg acc gag gcc gtg cag Lys Gly Ala His Thr Asn Asp Val Lys Gln Leu Thr Glu Ala Val Gln 515 520 525	1584
aag atc gcc acc gag tcc atc gtg atc tgg ggc aag act ccc aag ttc Lys Ile Ala Thr Glu Ser Ile Val Ile Trp Gly Lys Thr Pro Lys Phe 530 535 540	1632
aag ctg ccc atc cag aag gag acc tgg gag gcc tgg tgg acc gag tac Lys Leu Pro Ile Gln Lys Glu Thr Trp Glu Ala Trp Trp Thr Glu Tyr 545 550 555 560	1680
tgg cag gcc acc tgg atc ccc gag tgg gag ttc gtg aac acc ccc ccc Trp Gln Ala Thr Trp Ile Pro Glu Trp Glu Phe Val Asn Thr Pro Pro 565 570 575	1728
ctg gtg aag ctg tgg tac cag ctg gag aag gag ccc atc atc ggc gcc Leu Val Lys Leu Trp Tyr Gln Leu Glu Lys Glu Pro Ile Ile Gly Ala 580 585 590	1776
gag acc ttc tac gtg gac ggc gcc gcc aac cgc gag acc aag ctg ggc Glu Thr Phe Tyr Val Asp Gly Ala Ala Asn Arg Glu Thr Lys Leu Gly 595 600 605	1824
aag gcc ggc tac gtg acc gac cgc ggc cgc cag aag gtg gtg ccc ctg Lys Ala Gly Tyr Val Thr Asp Arg Gly Arg Gln Lys Val Val Pro Leu 610 615 620	1872
acc gac acc acc aac cag aag acc gag ctg cag gcc atc cac ctg gcc Thr Asp Thr Thr Asn Gln Lys Thr Glu Leu Gln Ala Ile His Leu Ala 625 630 635 640	1920
ctg caa gac tcc ggc ctg gag gtg aac atc gtg acc gac tcc cag tat Leu Gln Asp Ser Gly Leu Glu Val Asn Ile Val Thr Asp Ser Gln Tyr 645 650 655	1968
gca ttg ggc atc atc cag gcc cag ccc gac aag tcc gag tcc gag ctg Ala Leu Gly Ile Ile Gln Ala Gln Pro Asp Lys Ser Glu Ser Glu Leu 660 665 670	2016
gtg tcc cag atc atc gag cag ctg atc aag aag gag aag gtg tac ctg Val Ser Gln Ile Ile Glu Gln Leu Ile Lys Lys Glu Lys Val Tyr Leu 675 680 685	2064
gcc tgg gtg ccc gcc cac aag ggc atc ggc ggc aac gag cag gtg gac Ala Trp Val Pro Ala His Lys Gly Ile Gly Gly Asn Glu Gln Val Asp 690 695 700	2112
aag ctg gtg tcc gcc ggc atc cgc aag gtg ctg ttc ctg gac ggc atc Lys Leu Val Ser Ala Gly Ile Arg Lys Val Leu Phe Leu Asp Gly Ile 705 710 715 720	2160

gac aag gcc cag gag gag cac gag aag tac cac tcc aac tgg cgc gcc	2208
Asp Lys Ala Gln Glu Glu His Glu Lys Tyr His Ser Asn Trp Arg Ala	
725 730 735	
atg gcc tcc gac ttc aac ctg ccc ccc gtg gtg gcc aag gag atc gtg	2256
Met Ala Ser Asp Phe Asn Leu Pro Pro Val Val Ala Lys Glu Ile Val	
740 745 750	
gcc tcc tgc gac aag tgc cag ctg aag ggc gag gcc atg cac ggc cag	2304
Ala Ser Cys Asp Lys Cys Gln Leu Lys Gly Glu Ala Met His Gly Gln	
755 760 765	
gtg gac tgc tcc ccc ggc atc tgg cag ctg gac tgc acc cac ctg gag	2352
Val Asp Cys Ser Pro Gly Ile Trp Gln Leu Asp Cys Thr His Leu Glu	
770 775 780	
ggc aag gtg atc ctg gtg gcc gtg cac gtg gcc tcc ggc tac atc gag	2400
Gly Lys Val Ile Leu Val Ala Val His Val Ala Ser Gly Tyr Ile Glu	
785 790 795 800	
gcc gag gtg atc ccc gcc gag acc ggc cag gag acc gcc tac ttc ctg	2448
Ala Glu Val Ile Pro Ala Glu Thr Gly Gln Glu Thr Ala Tyr Phe Leu	
805 810 815	
ctg aag ctg gcc ggc cgc tgg ccc gtg aag acc gtg cac acc gac aac	2496
Leu Lys Leu Ala Gly Arg Trp Pro Val Lys Thr Val His Thr Asp Asn	
820 825 830	
ggc tcc aac ttc acc tcc acc acc gtg aag gcc gcc tgc tgg tgg gcc	2544
Gly Ser Asn Phe Thr Ser Thr Thr Val Lys Ala Ala Cys Trp Trp Ala	
835 840 845	
ggc atc aag cag gag ttc ggc atc ccc tac aac ccc cag tcc cag ggc	2592
Gly Ile Lys Gln Glu Phe Gly Ile Pro Tyr Asn Pro Gln Ser Gln Gly	
850 855 860	
gtg atc gag tcc atg aac aag gag ctg aag aag atc atc ggc caa gtc	2640
Val Ile Glu Ser Met Asn Lys Glu Leu Lys Lys Ile Ile Gly Gln Val	
865 870 875 880	
cgc gac cag gcc gag cac ctg aag acc gcc gtg cag atg gcc gtg ttc	2688
Arg Asp Gln Ala Glu His Leu Lys Thr Ala Val Gln Met Ala Val Phe	
885 890 895	
atc cac aac ttc aag cgc aag ggc ggc atc ggc ggc tac tcc gcc ggc	2736
Ile His Asn Phe Lys Arg Lys Gly Gly Ile Gly Gly Tyr Ser Ala Gly	
900 905 910	
gag cgc atc gtg gac atc atc gcc acc gac atc cag acc aag gag ctg	2784
Glu Arg Ile Val Asp Ile Ile Ala Thr Asp Ile Gln Thr Lys Glu Leu	
915 920 925	

cag aag cag atc acc aag atc cag aac ttc cgc gtg tac tac cgc gac	2832
Gln Lys Gln Ile Thr Lys Ile Gln Asn Phe Arg Val Tyr Tyr Arg Asp	
930 935 940	
tcc cgc gac ccc gtg tgg aag ggc ccc gcc aag ctg ctg tgg aag ggc	2880
Ser Arg Asp Pro Val Trp Lys Gly Pro Ala Lys Leu Leu Trp Lys Gly	
945 950 955 960	
gag ggc gcc gtg gtg atc cag gac aac tcc gac atc aag gtg gtg ccc	2928
Glu Gly Ala Val Val Ile Gln Asp Asn Ser Asp Ile Lys Val Val Pro	
965 970 975	
cgc cgc aag gcc aag atc atc cgc gac tac ggc aag cag atg gcc ggc	2976
Arg Arg Lys Ala Lys Ile Ile Arg Asp Tyr Gly Lys Gln Met Ala Gly	
980 985 990	
gac gac tgc gtg gcc tcc cgc cag gac gag gac taa	3012
Asp Asp Cys Val Ala Ser Arg Gln Asp Glu Asp *	
995 1000	

<210> 11  
 <211> 1003  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Codon optimized form of HIV pol coding region

<400> 11

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20 25 30	
Val Trp Gly Arg Asp Asn Asn Ser Leu Ser Glu Ala Gly Ala Asp Arg	
35 40 45	
Gln Gly Thr Val Ser Phe Ser Phe Pro Gln Ile Thr Leu Trp Gln Arg	
50 55 60	
Pro Leu Val Thr Ile Lys Ile Gly Gly Gln Leu Lys Glu Ala Leu Leu	
65 70 75 80	
Asp Thr Gly Ala Asp Asp Thr Val Leu Glu Glu Met Asn Leu Pro Gly	
85 90 95	
Arg Trp Lys Pro Lys Met Ile Gly Gly Ile Gly Gly Phe Ile Lys Val	
100 105 110	
Arg Gln Tyr Asp Gln Ile Leu Ile Glu Ile Cys Gly His Lys Ala Ile	
115 120 125	
Gly Thr Val Leu Val Gly Pro Thr Pro Val Asn Ile Ile Gly Arg Asn	
130 135 140	
Leu Leu Thr Gln Ile Gly Cys Thr Leu Asn Phe Pro Ile Ser Pro Ile	
145 150 155 160	
Glu Thr Val Pro Val Lys Leu Lys Pro Gly Met Asp Gly Pro Lys Val	
165 170 175	

Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	Lys	Ile	Lys	Ala	Leu	Val	Glu	Ile	180	185	190
Cys	Thr	Glu	Met	Glu	Lys	Glu	Gly	Lys	Ile	Ser	Lys	Ile	Gly	Pro	Glu	195	200	205
Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe	Ala	Ile	Lys	Lys	Lys	Asp	Ser	Thr	210	215	220
Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	225	230	235
Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	245	250	255
Gln	Lys	Lys	Ser	Val	Thr	Val	Leu	Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	260	265	270
Val	Pro	Leu	Asp	Lys	Asp	Phe	Arg	Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	275	280	285
Ser	Ile	Asn	Asn	Glu	Thr	Pro	Gly	Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	290	295	300
Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	Ala	Ile	Phe	Gln	Cys	Ser	Met	Thr	305	310	315
Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	Gln	Asn	Pro	Asp	Ile	Val	Ile	Tyr	325	330	335
Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val	Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	340	345	350
His	Arg	Thr	Lys	Ile	Glu	Glu	Leu	Arg	Gln	His	Leu	Leu	Arg	Trp	Gly	355	360	365
Phe	Thr	Thr	Pro	Asp	Lys	Lys	His	Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	370	375	380
Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	Lys	Trp	Thr	Val	Gln	Pro	Ile	Val	385	390	395
Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr	Val	Asn	Asp	Ile	Gln	Lys	Leu	Val	405	410	415
Gly	Lys	Leu	Asn	Trp	Ala	Ser	Gln	Ile	Tyr	Ala	Gly	Ile	Lys	Val	Arg	420	425	430
Gln	Leu	Cys	Lys	Leu	Leu	Arg	Gly	Thr	Lys	Ala	Leu	Thr	Glu	Val	Val	435	440	445
Pro	Leu	Thr	Glu	Glu	Ala	Glu	Leu	Glu	Leu	Ala	Glu	Asn	Arg	Glu	Ile	450	455	460
Leu	Lys	Glu	Pro	Val	His	Gly	Val	Tyr	Tyr	Asp	Pro	Ser	Lys	Asp	Leu	465	470	475
Ile	Ala	Glu	Ile	Gln	Lys	Gln	Gly	Gln	Gly	Gln	Trp	Thr	Tyr	Gln	Ile	485	490	495
Tyr	Gln	Glu	Pro	Phe	Lys	Asn	Leu	Lys	Thr	Gly	Lys	Tyr	Ala	Arg	Met	500	505	510
Lys	Gly	Ala	His	Thr	Asn	Asp	Val	Lys	Gln	Leu	Thr	Glu	Ala	Val	Gln	515	520	525
Lys	Ile	Ala	Thr	Glu	Ser	Ile	Val	Ile	Trp	Gly	Lys	Thr	Pro	Lys	Phe	530	535	540
Lys	Leu	Pro	Ile	Gln	Lys	Glu	Thr	Trp	Glu	Ala	Trp	Trp	Thr	Glu	Tyr	545	550	555
Trp	Gln	Ala	Thr	Trp	Ile	Pro	Glu	Trp	Glu	Phe	Val	Asn	Thr	Pro	Pro	565	570	575
Leu	Val	Lys	Leu	Trp	Tyr	Gln	Leu	Glu	Lys	Glu	Pro	Ile	Ile	Gly	Ala	580	585	590

Glu	Thr	Phe	Tyr	Val	Asp	Gly	Ala	Ala	Asn	Arg	Glu	Thr	Lys	Leu	Gly
		595					600					605			
Lys	Ala	Gly	Tyr	Val	Thr	Asp	Arg	Gly	Arg	Gln	Lys	Val	Val	Pro	Leu
	610					615					620				
Thr	Asp	Thr	Thr	Asn	Gln	Lys	Thr	Glu	Leu	Gln	Ala	Ile	His	Leu	Ala
625					630					635					640
Leu	Gln	Asp	Ser	Gly	Leu	Glu	Val	Asn	Ile	Val	Thr	Asp	Ser	Gln	Tyr
				645					650					655	
Ala	Leu	Gly	Ile	Ile	Gln	Ala	Gln	Pro	Asp	Lys	Ser	Glu	Ser	Glu	Leu
			660				665						670		
Val	Ser	Gln	Ile	Ile	Glu	Gln	Leu	Ile	Lys	Lys	Glu	Lys	Val	Tyr	Leu
		675					680					685			
Ala	Trp	Val	Pro	Ala	His	Lys	Gly	Ile	Gly	Gly	Asn	Glu	Gln	Val	Asp
	690					695					700				
Lys	Leu	Val	Ser	Ala	Gly	Ile	Arg	Lys	Val	Leu	Phe	Leu	Asp	Gly	Ile
705					710					715					720
Asp	Lys	Ala	Gln	Glu	Glu	His	Glu	Lys	Tyr	His	Ser	Asn	Trp	Arg	Ala
				725					730					735	
Met	Ala	Ser	Asp	Phe	Asn	Leu	Pro	Pro	Val	Val	Ala	Lys	Glu	Ile	Val
			740					745					750		
Ala	Ser	Cys	Asp	Lys	Cys	Gln	Leu	Lys	Gly	Glu	Ala	Met	His	Gly	Gln
		755					760					765			
Val	Asp	Cys	Ser	Pro	Gly	Ile	Trp	Gln	Leu	Asp	Cys	Thr	His	Leu	Glu
	770					775					780				
Gly	Lys	Val	Ile	Leu	Val	Ala	Val	His	Val	Ala	Ser	Gly	Tyr	Ile	Glu
785					790					795					800
Ala	Glu	Val	Ile	Pro	Ala	Glu	Thr	Gly	Gln	Glu	Thr	Ala	Tyr	Phe	Leu
				805					810					815	
Leu	Lys	Leu	Ala	Gly	Arg	Trp	Pro	Val	Lys	Thr	Val	His	Thr	Asp	Asn
			820					825					830		
Gly	Ser	Asn	Phe	Thr	Ser	Thr	Thr	Val	Lys	Ala	Ala	Cys	Trp	Trp	Ala
		835					840					845			
Gly	Ile	Lys	Gln	Glu	Phe	Gly	Ile	Pro	Tyr	Asn	Pro	Gln	Ser	Gln	Gly
	850					855					860				
Val	Ile	Glu	Ser	Met	Asn	Lys	Glu	Leu	Lys	Lys	Ile	Ile	Gly	Gln	Val
865					870					875					880
Arg	Asp	Gln	Ala	Glu	His	Leu	Lys	Thr	Ala	Val	Gln	Met	Ala	Val	Phe
				885					890					895	
Ile	His	Asn	Phe	Lys	Arg	Lys	Gly	Gly	Ile	Gly	Gly	Tyr	Ser	Ala	Gly
			900					905					910		
Glu	Arg	Ile	Val	Asp	Ile	Ile	Ala	Thr	Asp	Ile	Gln	Thr	Lys	Glu	Leu
		915					920					925			
Gln	Lys	Gln	Ile	Thr	Lys	Ile	Gln	Asn	Phe	Arg	Val	Tyr	Tyr	Arg	Asp
	930					935					940				
Ser	Arg	Asp	Pro												



<210> 12  
 <211> 8908  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Packaging construct pHDmHgpm2 comprising a codon  
 optimized form of HIV gag pol region

<400> 12

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cgggggtcatt	agttcatagc	ccatatatgg	agttccgcgt	tacataactt	acggtaaagt	180
gcccgcctgg	ctgaccgccc	aacgaccccc	gcccattgac	gtcaataatg	acgtatgttc	240
ccatagtaac	gccaataggg	actttccatt	gacgtcaatg	ggtggagtat	ttacggtaaa	300
ctgcccactt	ggcagtagat	caagtgtatc	atatgccaag	tacgccccct	attgacgtca	360
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cttggcagta	catctacgta	ttagtcatcg	ctattacat	ggtgatgcgg	ttttggcagt	480
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